

**Amendments to Specification****Paragraph at page 5, lines 20-35:**

Figures 1A-1D shows a comparison of the amino acid sequences of the *Arabidopsis thaliana* glutamine amidotransferase protein having NCBI General Identifier No. 3219164 (SEQ ID NO:15) and the amino acid sequence encoded by the cDNA insert in clone ids.pk0024.c4 (SEQ ID NO:2) encoding an entire glutamine amidotransferase (HisHF) and the amino acid sequences encoding partial glutamine amidotransferases (HisHF) from corn contig assembled from clones cpelc.pk012.c10, p0010.cbpbq28r, and p0131.ccdap46r (SEQ ID NO:4), corn contig assembled from clones cco1n.pk071.i21, cco1n.pk071.i21:fis, cpj1c.pk005.p14, p0016.ctscc75r, and rlr48.pk0001.f5 (SEQ ID NO:6), corn clone p0119.cmtnx82r (SEQ ID NO:8), rice clone rr1.pk094.n24 (SEQ ID NO:10), soybean clone sdp4c.pk002.n13 (SEQ ID NO:12), and a soybean contig assembled from clones sl1.pk152.c18, sl1.pk152.c18:fis, and src3c.pk022.b14 (SEQ ID NO:14). The predicted CTP cleavage site is indicated with an arrow above the sequences. ~~The, the~~ carbamoyl-phosphate synthase protein GATASE domain signature E motif 2 and the GATASE type 1 motif are boxed. An asterisk (\*) above the alignment indicates those amino acids conserved among impatiens and Arabidopsis sequences. The location of the amino acids which ~~were~~when mutagenized ~~without~~ effected ~~on the~~ enzyme activity are indicated by a ~~gray~~black box and white letters. Dashes are used by the program to maximize the alignment.

**Paragraph at page 22, lines 5-13:**

Figure 1 presents an alignment of the amino acid sequences set forth in SEQ ID NO:2 and the *Arabidopsis thaliana* sequence (SEQ ID NO:15) and the amino acid sequences from corn contig assembled from clones cpe1c.pk012.c10, p0010.cbpbq28r, and p0131.ccdap46r (SEQ ID NO:4), corn contig assembled from clones cco1n.pk071.i21, cco1n.pk071.i21:fis, cpj1c.pk005.p14, p0016.ctscc75r, and rlr48.pk0001.f5 (SEQ ID NO:6), corn clone p0119.cmtnx82r (SEQ ID NO:8), rice clone rr1.pk094.n24 (SEQ ID NO:10), soybean clone sdp4c.pk002.n13 (SEQ ID NO:12), and soybean contig assembled from clones sl1.pk152.c18, sl1.pk152.c18:fis, and src3c.pk022.b14 (SEQ ID NO:14). Indicated with an arrow above the sequences is the location of the predicted CTP cleavage site. Boxed are the carbamoyl-phosphate synthase protein GATASE domain signature E motif 2 (probably containing the active Cysteine) and the GTASE type 1 domain. An asterisk (\*) above the alignment indicates those amino acids conserved among both the impatiens and Arabidopsis sequences. The location of the amino acids which when mutagenized effected enzyme activity are indicated by a grayblack box and white letters.~~An x above the sequence indicates amino acids which when mutated diminish the function of the enzymes and an equal sign (=) above the alignment indicates the amino acids which when mutated do not appear to effect the activity of the enzyme.~~